Clean Copy of All Pending Claims

1. A method for detecting the presence of at least one selected strain of an organism in a sample, comprising the steps of:

providing a sample that may comprise nucleic acid from at least one selected strain of an organism and nucleic acid from at least one non-selected strain of the organism;

providing a plurality of primers substantially complementary to regions of both said nucleic acid from at least one selected strain of the organism and said nucleic acid from at least one non-selected strain of the organism;

exposing said sample to at least one probe that is sufficiently complementary to a portion of said nucleic acid from at least one non-selected strain to block full length amplification of said nucleic acid from at least one non-selected strain between said plurality of primers, said at least one probe comprising a nucleic acid analog;

amplifying said nucleic acid from at least one selected strain between said plurality of primers; and

detecting amplification product of nucleic acid from at least one selected strain.

2. The method of claim 1, wherein said at least one selected strain comprises a pathogenic strain.

3. The method of claim 2, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.

4. The method of claim 1, wherein said organism comprises human papilloma virus (HPV).

5. The method of claim 1, wherein said at least one probe comprises PNA.

6. The method of claim 5, wherein said at least one probe further comprises a nucleotide different from PNA.

7. The method of claim 1, wherein each of said at least one probe comprises at least 8 bases.

8. The method of claim 1, wherein the step of amplifying said nucleic acid of at least one selected strain between said plurality of primers comprises conducting a reaction selected from the group consisting of a polymerase chain reaction, a ligase chain reaction, a rolling circle replication, a branched chain amplification, a nucleic acid based sequence amplification (NASBA), a Cleavase Fragment Length Polymorphism, ICAN and RAM .

9. The method of claim 4, wherein said regions of both said nucleic acids are parts of a region selected from the group consisting of L1, L2, E1, E6, and E7 region.

10. The method of claim 4, wherein said at least one non-selected strain equals all the low-risk HPV strains known.

11. The method of claim 4, wherein said at least one non-selected strain is selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

12. The method of claim 4, wherein said at least one selected strain comprises a plurality of high-risk HPV strains.

13. The method of claim 4, wherein said plurality of primers comprise MY09 and MY11 (SEQ. ID. NOS. 10 and 11).

14. The method of claim 4, wherein said at least one probe is selected from the group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7.

15. The method of claim 1, wherein said sample is a cervical scraping.

16. The method of claim 1, wherein said step of detecting amplification product comprises in-gel electrophoresis of said product and staining said product with ethidium bromide.

17-37. Canceled.